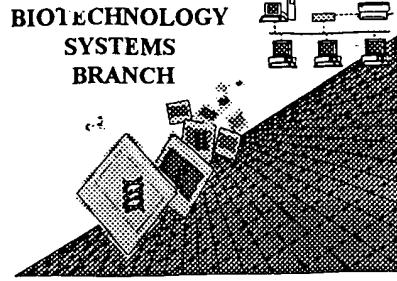


RAW SEQUENCE LISTING

ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/903,188

Source: O/PE

Date Processed by STIC: 7/26/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	SERIAL NUMBER: <u>09/903,188</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 <input type="checkbox"/> Wrapped Nucleic Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 <input checked="" type="checkbox"/> Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 <input checked="" type="checkbox"/> Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 <input type="checkbox"/> Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 <input type="checkbox"/> Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 <input type="checkbox"/> PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped	
	Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If Intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 <input type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 <input type="checkbox"/> Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 <input type="checkbox"/> Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 <input type="checkbox"/> PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 <input type="checkbox"/> Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.	

OIPE

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/903,188

DATE: 07/26/2001
 TIME: 14:58:54

Input Set : A:\seqlist.txt
 Output Set: N:\CRF3\07262001\I903188.raw

Does Not Comply
 Corrected Diskette Needed

SEQUENCE LISTING

5 (1) GENERAL INFORMATION:

7 (i) APPLICANT: De Robertis, Edward M.
 8 Bouwmeester, Tewis

10 (ii) TITLE OF INVENTION: Endoderm, Cardiac and Neural Inducing
 11 Factors

13 (iii) NUMBER OF SEQUENCES: 10

15 (iv) CORRESPONDENCE ADDRESS:

16 (A) ADDRESSEE: Majestic, Parsons, Siebert & Hsue
 17 (B) STREET: Four Embarcadero Center, Suite 1100

18 (C) CITY: San Francisco

19 (D) STATE: California

20 (E) COUNTRY: U.S.A.

21 (F) ZIP: 94111-4106

23 (v) COMPUTER READABLE FORM:

24 (A) MEDIUM TYPE: Floppy disk

25 (B) COMPUTER: IBM PC compatible

26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

29 (vi) CURRENT APPLICATION DATA:

30 (A) APPLICATION NUMBER: US/09/903,188

31 (B) FILING DATE: 11-Jul-2001

32 (C) CLASSIFICATION:

34 (vii) PRIOR APPLICATION DATA:

35 (A) APPLICATION NUMBER: US 60/020,150

36 (B) FILING DATE: 20-JUN-1996

38 (viii) ATTORNEY/AGENT INFORMATION:

39 (A) NAME: Siebert, J. Suzanne

40 (B) REGISTRATION NUMBER: 28,758

41 (C) REFERENCE/DOCKET NUMBER: 3100.002US1

43 (ix) TELECOMMUNICATION INFORMATION:

44 (A) TELEPHONE: 415/248-5500

45 (B) TELEFAX: 415/362-5418

ERRORED SEQUENCES

330 (2) INFORMATION FOR SEQ ID NO: 5:

332 (i) SEQUENCE CHARACTERISTICS: 707 (p.3)

333 (A) LENGTH: 979 amino acids

334 (B) TYPE: amino acid

335 (D) TOPOLOGY: linear

337 (ii) MOLECULE TYPE: peptide

339 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

341 Met Leu Leu Leu Phe Arg Ala Ile Pro Met Leu Leu Gly Leu Met

342 1 5 10 15

344 Val Leu Gln Thr Asp Cys Glu Ile Ala Gln Tyr Tyr Ile Asp Glu

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/903,188

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Input Set : A:\seqlist.txt
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345	20	25	30	
347	Glu Pro Pro Gly Thr Val Ile Ala Val Leu Ser Gln His Ser Ile Phe			
348	35	40	45	
350	Asn Thr Thr Asp Ile Pro Ala Thr Asn Phe Arg Leu Met Lys Gln Phe			
351	50	55	60	
353	Asn Asn Ser Leu Ile Gly Val Arg Glu Ser Asp Gly Gln Leu Ser Ile			
354	65	70	75	80
356	Met Glu Arg Ile Asp Arg Glu Gln Ile Cys Arg Gln Ser Leu His Cys			
357	85	90	95	
359	Asn Leu Ala Leu Asp Val Val Ser Phe Ser Lys Gly His Phe Lys Leu			
360	100	105	110	
362	Leu Asn Val Lys Val Glu Val Arg Asp Ile Asn Asp His Ser Pro His			
363	115	120	125	
365	Phe Pro Ser Glu Ile Met His Val Glu Val Ser Glu Ser Ser Ser Val			
366	130	135	140	
368	Gly Thr Arg Ile Pro Leu Glu Ile Ala Ile Asp Glu Asp Val Gly Ser			
369	145	150	155	160
371	Asn Ser Ile Gln Asn Phe Gln Ile Ser Asn Asn Ser His Phe Ser Ile			
372	165	170	175	
374	Asp Val Leu Thr Arg Ala Asp Gly Val Lys Tyr Ala Asp Leu Val Leu			
375	180	185	190	
377	Met Arg Glu Leu Asp Arg Glu Ile Gln Pro Thr Tyr Ile Met Glu Leu			
378	195	200	205	
380	Leu Ala Met Asp Gly Gly Val Pro Ser Leu Ser Gly Thr Ala Val Val			
381	210	215	220	
383	Asn Ile Arg Val Leu Asp Phe Asn Asp Asn Ser Pro Val Phe Glu Arg			
384	225	230	235	240
386	Ser Thr Ile Ala Val Asp Leu Val Glu Asp Ala Pro Leu Gly Tyr Leu			
387	245	250	255	
389	Leu Leu Glu Leu His Ala Thr Asp Asp Asp Glu Gly Val Asn Gly Glu			
390	260	265	270	
392	Ile Val Tyr Gly Phe Ser Thr Leu Ala Ser Gln Glu Val Arg Gln Leu			
393	275	280	285	
395	Phe Lys Ile Asn Ser Arg Thr Gly Ser Val Thr Leu Glu Gly Gln Val			
396	290	295	300	
398	Asp Phe Glu Thr Lys Gln Thr Tyr Glu Phe Glu Val Gln Ala Gln Asp			
399	305	310	315	320
401	Leu Gly Pro Asn Pro Leu Thr Ala Thr Cys Lys Val Thr Val His Ile			
402	325	330	335	
404	Leu Asp Val Asn Asp Asn Thr Pro Ala Ile Thr Ile Thr Pro Leu Thr			
405	340	345	350	
407	Thr Val Asn Ala Gly Val Ala Tyr Ile Pro Glu Thr Ala Thr Lys Glu			
408	355	360	365	
410	Asn Phe Ile Ala Leu Ile Ser Thr Thr Asp Arg Ala Ser Gly Ser Asn			
411	370	375	380	
413	Gly Gln Val Arg Cys Thr Leu Tyr Gly His Glu His Phe Lys Leu Gln			
414	385	390	395	400
416	Gln Ala Tyr Glu Asp Ser Tyr Met Ile Val Thr Thr Ser Thr Leu Asp			
417	405	410	415	

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/903,188

DATE: 07/26/2001
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Input Set : A:\seqlist.txt
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419 Arg Glu Asn Ile Ala Ala Tyr Ser Leu Thr Val Val Ala Glu Asp Leu
 420 420 425 430
 422 Gly Phe Pro Ser Leu Lys Thr Lys Lys Tyr Tyr Thr Val Lys Val Ser
 423 435 440 445
 425 Asp Glu Asn Asp Asn Ala Pro Val Phe Ser Lys Pro Gln Tyr Glu Ala
 426 450 455 460
 428 Ser Ile Leu Glu Asn Asn Ala Pro Gly Ser Tyr Ile Thr Thr Val Ile
 429 465 470 475 480
 431 Ala Arg Asp Ser Asp Ser Asp Gln Asn Gly Lys Val Asn Tyr Arg Leu
 432 485 490 495
 434 Val Asp Ala Lys Val Met Gly Gln Ser Leu Thr Thr Phe Val Ser Leu
 435 500 505 510
 437 Asp Ala Asp Ser Gly Val Leu Arg Ala Val Arg Ser Leu Asp Tyr Glu
 438 515 520 525
 440 Lys Leu Lys Gln Leu Asp Phe Glu Ile Glu Ala Ala Asp Asn Gly Ile
 441 530 535 540
 443 Pro Gln Leu Ser Thr Arg Val Gln Leu Asn Leu Arg Ile Val Asp Gln
 444 545 550 555 560
 446 Asn Asp Asn Cys Pro Val Ile Thr Asn Pro Leu Leu Asn Asn Gly Ser
 447 565 570 575
 449 Gly Glu Val Leu Leu Pro Ile Ser Ala Pro Gln Asn Tyr Leu Val Phe
 450 580 585 590
 452 Gln Leu Lys Ala Glu Asp Ser Asp Glu Gly His Asn Ser Gln Leu Phe
 453 595 600 605
 455 Tyr Thr Ile Leu Arg Asp Pro Ser Arg Leu Phe Ala Ile Asn Lys Glu
 456 610 615 620
 458 Ser Gly Glu Val Phe Leu Lys Lys Gln Leu Asn Ser Asp His Ser Glu
 459 625 630 635 640
 461 Asp Leu Ser Ile Val Val Ala Val Tyr Asp Leu Gly Arg Pro Ser Leu
 462 645 650 655
 464 Val Ala Asn Arg Met His Ala Glu Tyr Glu Arg Asp Leu Val Asn Arg
 E--> 465 ~~930~~ 660 ~~935~~ 665 ~~940~~ 670
 467 Ser Ala Thr Leu Ser Pro Gln Arg Ser Ser Ser Arg Tyr Gln Glu Phe
 E--> 468 ~~945~~ 675 ~~950~~ 680 ~~955~~ 685 ~~960~~
 470 Asn Tyr Ser Pro Gln Ile Ser Arg Gln Leu His Pro Ser Glu Ile Ala
 E--> 471 690 695 695 690 700 700
 E--> 473 Thr Thr Phe ~~705~~
 780 (2) INFORMATION FOR SEQ ID NO: 9:
 782 (i) SEQUENCE CHARACTERISTICS:
 783 (A) LENGTH: 325 amino acids
 784 (B) TYPE: amino acid
 785 (D) TOPOLOGY: linear
 787 (ii) MOLECULE TYPE: peptide
 789 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
 791 Met Val Cys Gly Ser Pro Gly Gly Met Leu Leu Leu Arg Ala Gly Leu
 E--> 792 1 5 ~~10~~ 10 15
 794 Leu Ala Leu Ala Ala Leu Cys Leu Leu Arg Val Pro Gly Ala Arg Ala
 795 20 25 30
 797 Ala Ala Cys Glu Pro Val Arg Ile Pro Leu Cys Lys Ser Leu Pro Trp

Mesalysine
amino acid has.
(see item 3)
in Exam
Summary
Sheet)

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/903,188

DATE: 07/26/2001
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Input Set : A:\seqlist.txt
 Output Set: N:\CRF3\07262001\I903188.raw

798	35	40	45
800	Asn Met Thr Lys Met Pro Asn His Leu His His Ser Thr Gln Ala Asn		
801	50	55	60
803	Ala Ile Leu Ala Ile Glu Gln Phe Glu Gly Leu Leu Gly Thr His Cys		
804	65	70	75
806	Ser Pro Asp Leu Leu Phe Phe Leu Cys Ala Met Tyr Ala Pro Ile Cys		80
807	85	90	95
809	Thr Ile Asp Phe Gln His Glu Pro Ile Lys Pro Cys Lys Ser Val Cys		
810	100	105	110
812	Glu Arg Ala Arg Gln Gly Cys Glu Pro Ile Leu Ile Lys Tyr Arg His		
813	115	120	125
815	Ser Trp Pro Glu Asn Leu Ala Cys Glu Glu Leu Pro Val Tyr Asp Arg		
816	130	135	140
818	Gly Val Cys Ile Ser Pro Glu Ala Ile Val Thr Ala Asp Gly Ala Asp		
819	145	150	155
821	Phe Pro Met Asp Ser Ser Asn Gly Asn Cys Arg Gly Ala Ser Ser Glu		160
822	165	170	175
824	Arg Cys Lys Cys Lys Pro Ile Arg Ala Thr Gln Lys Thr Tyr Phe Arg		
825	180	185	190
827	Asn Asn Tyr Asn Tyr Val Ile Arg Ala Lys Val Lys Glu Ile Lys Thr		
828	195	200	205
830	Lys Cys His Asp Val Thr Ala Val Val Glu Val Lys Glu Ile Leu Lys		
831	210	215	220
833	Ser Ser Leu Val Asn Ile Pro Arg Asp Thr Val Asn Leu Tyr Thr Ser		
834	225	230	235
836	Ser Gly Cys Leu Cys Pro Pro Leu Asn Val Asn Glu Glu Tyr Ile Ile		240
837	245	250	255
839	Met Gly Tyr Glu Asp Glu Glu Arg Ser Arg Leu Leu Leu Val Glu Gly		
840	260	265	270
842	Ser Ile Ala Glu Lys Trp Lys Asp Arg Leu Gly Lys Lys Val Lys Arg		
843	275	280	285
845	Trp Asp Met Lys Leu Arg His Leu Gly Leu Ser Lys Ser Asp Ser Ser		
846	290	295	300
848	Asn Ser Asp Ser Thr Gln Ser Gln Lys Ser Gly Arg Asn Ser Asn Pro		
849	305	310	315
851	Arg Gln Ala Arg Asn		320
852	325		

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/903,188

DATE: 07/26/2001
TIME: 14:58:55

Input Set : A:\seqlist.txt
Output Set: N:\CRF3\07262001\I903188.raw

L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:465 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:5
M:332 Repeated in SeqNo=5
L:473 M:203 E: No. of Seq. differs, LENGTH:Input:979 Found:707 SEQ:5
L:792 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:9